PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/635,864*

DATE: 10/05/2000
TIME: 01:46:19

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This Raw Listing contains the General
Information Section and up to the first 5 pages.

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 1                            SEQUENCE LISTING
 2
 3   (1)    General Information:
 4
 5        (i) APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA, MARGHERITA
 6
 7       (ii) TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS
 8
 9      (iii) NUMBER OF SEQUENCES: 99
10
11       (iv) CORRESPONDENCE ADDRESS:
12            (A) ADDRESSEE: Klauber & Jackson
13            (B) STREET: 411 Hackensack Avenue
14            (C) CITY: Hackensack
15            (D) STATE: New Jersey
16            (E) COUNTRY: USA
17            (F) ZIP: 07601
18
19        (v) COMPUTER READABLE FORM:
20            (A) MEDIUM TYPE: Floppy disk
21            (B) COMPUTER: IBM PC compatible
22            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
23            (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
24
25       (vi) CURRENT APPLICATION DATA:
26            (A) APPLICATION NUMBER: 09/635,864
27            (B) FILING DATE: August 10, 2000
28            (C) CLASSIFICATION:
29
30      (vii) PRIOR APPLICATION DATA:
31            (A) APPLICATION NUMBER: 08/438,431
32            (B) FILING DATE: May 10, 1995
33            (C) CLASSIFICATION:
34
35      (vii) PRIOR APPLICATION DATA:
36            (A) APPLICATION NUMBER: 08/347,563
37            (B) FILING DATE: November 30, 1994
38            (C) CLASSIFICATION:
39
40      (vii) PRIOR APPLICATION DATA:
41            (A) APPLICATION NUMBER: 08/292,345
42            (B) FILING DATE: August 17, 1994
43            (C) CLASSIFICATION:
44
45     (viii) ATTORNEY/AGENT INFORMATION:
46            (A) NAME: Jackson Esq., David A.
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47              (B) REGISTRATION NUMBER: 26,742
48              (C) REFERENCE/DOCKET NUMBER: 600-1-087 CIP1
49
50       (ix) TELECOMMUNICATION INFORMATION:
51              (A) TELEPHONE: 201 487-5800
52              (B) TELEFAX: 201 343-1684
53              (C) TELEX: 133521
54
55   (2) INFORMATION FOR SEQ ID NO:1:
56
57       (i) SEQUENCE CHARACTERISTICS:
58              (A) LENGTH: 2793 base pairs
59              (B) TYPE: nucleic acid
60              (C) STRANDEDNESS: double
61              (D) TOPOLOGY: linear
62
63      (ii) MOLECULE TYPE: DNA (genomic)
64              (A) DESCRIPTION: Murine ob cDNA
65
66     (iii) HYPOTHETICAL: NO
67
68      (iv) ANTI-SENSE: NO
69
70      (vi) ORIGINAL SOURCE:
71              (A) ORGANISM: Murine
72
73      (ix) FEATURE:
74              (A) NAME/KEY: CDS
75              (B) LOCATION: 57..560
76
77
78      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
79
80   GGATCCCTGC TCCAGCAGCT GCAAGGTGCA AGAAGAAGAA GATCCCAGGG AGGAAA              56
81
82   ATG TGC TGG AGA CCC CTG TGT CGG TTC CTG TGG CTT TGG TCC TAT CTG           104
83   Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
84    1               5                   10                  15
85
86   TCT TAT GTT CAA GCA GTG CCT ATC CAG AAA GTC CAG GAT GAC ACC AAA           152
87   Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
88               20                  25                  30
89
90   ACC CTC ATC AAG ACC ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG           200
91   Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
92               35                  40                  45
93
94   CAG TCG GTA TCC GCC AAG CAG AGG GTC ACT GGC TTG GAC TTC ATT CCT           248
95   Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
96           50                  55                  60
97
98   GGG CTT CAC CCC ATT CTG AGT TTG TCC AAG ATG GAC CAG ACT CTG GCA           296
99   Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
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103   Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln
104                   85                  90                  95
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106   ATA GCC AAT GAC CTG GAG AAT CTC CGA GAC CTC CTC CAT CTG CTG GCC        392
107   Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
108               100                 105                 110
109
110   TTC TCC AAG AGC TGC TCC CTG CCT CAG ACC AGT GGC CTG CAG AAG CCA        440
111   Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro
112           115                 120                 125
113
114   GAG AGC CTG GAT GGC GTC CTG GAA GCC TCA CTC TAC TCC ACA GAG GTG        488
115   Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val
116       130                 135                 140
117
118   GTG GCT TTG AGC AGG CTG CAG GGC TCT CTG CAG GAC ATT CTT CAA CAG        536
119   Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln
120   145                 150                 155                 160
121
122   TTG GAT GTT AGC CCT GAA TGC TGA AGTTTCAAAG GCCACCAGGC TCCCAAGA        588
123   Leu Asp Val Ser Pro Glu Cys  *
124                   165
125
126   ATCATGTAGA GGGAAGAAAC CTTGGCTTCC AGGGGTCTTC AGGAGAAGAG AGCCATGTGC       648
127
128   ACACATCCAT CATTCATTTC TCTCCCTCCT GTAGACCACC CATCCAAAGG CATGACTCCA       708
129
130   CAATGCTTGA CTCAAGTTAT CCACACAACT TCATGAGCAC AAGGAGGGGC CAGCCTGCAG       768
131
132   AGGGGACTCT CACCTAGTTC TTCAGCAAGT AGAGATAAGA GCCATCCCAT CCCCTCCATG       828
133
134   TCCCACCTGC TCCGGGTACA TGTTCCTCCG TGGGTACACG CTTCGCTGCG GCCCAGGAGA       888
135
136   GGTGAGGTAG GGATGGGTAG AGCCTTTGGG CTGTCTCAGA GTCTTTGGGA GCACCGTGAA       948
137
138   GGCTGCATCC ACACACAGCT GGAAACTCCC AAGCAGCACA CGATGGAAGC ACTTATTTAT      1008
139
140   TTATTCTGCA TTCTATTTTG GATGGATCTG AAGCAAGGCA TCAGCTTTTT CAGGCTTTGG      1068
141
142   GGGTCAGCCA GGATGAGGAA GGCTCCTGGG GTGCTGCTTT CAATCCTATT GATGGGTCTG      1128
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144   CCCGAGGCAA ACCTAATTTT TGAGTGACTG GAAGGAAGGT TGGGATCTTC CAAACAAGAG      1188
145
146   TCTATGCAGG TAGCGCTCAA GATTGACCTC TGGTGACTGG TTTTGTTTCT ATTGTGACTG      1248
147
148   ACTCTATCCA AACACGTTTG CAGCGGCATT GCCGGGAGCA TAGGCTAGGT TATTATCAAA      1308
149
150   AGCAGATGAA TTTTGTCAAG TGTAATATGT ATCTATGTGC ACCTGAGGGT AGAGGATGTG      1368
151
152   TTAGAGGGAG GGTGAAGGAT CCGGAAGTGT TCTCTGAATT ACATATGTGT GGTAGGCTTT      1428
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154   TCTGAAAGGG TGAGGCATTT TCTTACCTCT GTGGCCACAT AGTGTGGCTT TGTGAAAAGG   1488
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156   ACAAAGGAGT TGACTCTTTC CGGAACATTT GGAGTGTACC AGGCACCCTT GGAGGGGCTA   1548
157
158   AAGCTACAGG CCTTTTGTTG GCATATTGCT GAGCTCAGGG AGTGAGGGCC CCACATTTGA   1608
159     .
160   GACAGTGAGC CCCAAGAAAA GGGTCCCTGG TGTAGATCTC CAAGGTTGTC CAGGGTTGAT   1668
161
162   CTCACAATGC GTTTCTTAAG CAGGTAGACG TTTGCATGCC AATATGTGGT TCTCATCTGA   1728
163
164   TTGGTTCATC CAAAGTAGAA CCCTGTCTCC CACCCATTCT GTGGGGAGTT TTGTTCCAGT   1788
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166   GGGAATGAGA AATCACTTAG CAGATGGTCC TGAGCCCTGG GCCAGCACTG CTGAGGAAGT   1848
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168   GCCAGGGCCC CAGGCCAGGC TGCCAGAATT GCCCTTCGGG CTGGAGGATG AACAAAGGGG   1908
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170   CTTGGGTTTT TCCATCACCC CTGCACCCTA TGTCACCATC AAACTGGGGG GCAGATCAGT   1968
171
172   GAGAGGACAC TTGATGGAAA GCAATACACT TTAAGACTGA GCACAGTTTC GTGCTCAGCT   2028
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174   CTGTCTGGTG CTGTGAGCTA GAGAAGCTCA CCACATACAT ATAAAAATCA GAGGCTCATG   2088
175
176   TCCCTGTGGT TAGACCCTAC TCGCGGCGGT GTACTCCACC ACAGCAGCAC CGCACCGCTG   2148
177
178   GAAGTACAGT GCTGTCTTCA ACAGGTGTGA AAGAACCTGA GCTGAGGGTG ACAGTGCCCA   2208
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180   GGGGAACCCT GCTTGCAGTC TATTGCATTT ACATACCGCA TTTCAGGGCA CATTAGCATC   2268
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182   CACTCCTATG GTAGCACACT GTTGACAATA GGACAAGGGA TAGGGGTTGA CTATCCCTTA   2328
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184   TCCAAAATGC TTGGGACTAG AAGAGTTTTG GATTTTAGAG TCTTTTCAGG CATAGGTATA   2388
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186   TTTGAGTATA TATAAAATGA GATATCTTGG GGATGGGGCC CAAGTATAAA CATGAAGTTC   2448
187
188   ATTTATATTT CATAATACCG TATAGACACT GCTTGAAGTG TAGTTTTATA CAGTGTTTTA   2508
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190   AATAACGTTG TATGCATGAA AGACGTTTTT ACAGCATGAA CCTGTCTACT CATGCCAGCA   2568
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192   CTCAAAAACC TTGGGGTTTT GGAGCAGTTT GGATCTTGGG TTTTCTGTTA AGAGATGGTT   2628
193
194   AGCTTATACC TAAAACCATA ATGGCAAACA GGCTGCAGGA CCAGACTGGA TCCTCAGCCC   2688
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196   TGAAGTGTGC CCTTCCAGCC AGGTCATACC CTGTGGAGGT GAGCGGGATC AGGTTTTGTG   2748
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198   GTGCTAAGAG AGGAGTTGGA GGTAGATTTT GGAGGATCTG AGGGC                    2793
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201   (2) INFORMATION FOR SEQ ID NO:2:
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203          (i) SEQUENCE CHARACTERISTICS:
204               (A) LENGTH: 167 amino acids
205               (B) TYPE: amino acid
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206                     (D) TOPOLOGY: linear
207
208           (ii) MOLECULE TYPE: protein
209                   (A) DESCRIPTION: Murine ob polypeptide
210
211           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
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213   Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
214    1               5                  10                  15
215
216   Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
217               20                  25                  30
218
219   Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
220           35                  40                  45
221
222   Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
223       50                  55                  60
224
225   Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
226    65                  70                  75                  80
227
228   Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln
229               85                  90                  95
230
231   Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
232           100                 105                 110
233
234   Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro
235           115                 120                 125
236
237   Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val
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243   Leu Asp Val Ser Pro Glu Cys
244                   165
245
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247   (2) INFORMATION FOR SEQ ID NO:3:
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249           (i) SEQUENCE CHARACTERISTICS:
250               (A) LENGTH: 700 base pairs
251               (B) TYPE: nucleic acid
252               (C) STRANDEDNESS: double
253               (D) TOPOLOGY: linear
254
255           (ii) MOLECULE TYPE: cDNA
256               (A) DESCRIPTION: Human ob cDNA where N represents any nucleotide
257
258           (iii) HYPOTHETICAL: NO
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/635,864*

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